RAW SEQUENCE LISTING                    DATE: 03/29/2001
PATENT APPLICATION:  US/09/646,825      TIME: 15:59:57

Input Set : A:\55022715.app
Output Set: N:\CRF3\03292001\I646825.raw

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 3 <110> APPLICANT: MORI, SATOSHI
 4        NAKANISHI, HIROMI
 5        OKI, HIROYUKI
 6        YAMAGUCHI, HIROTAKA
 8 <120> TITLE OF INVENTION: METHOD FOR TRANSFORMING PLANT, THE RESULTANT PLANT AND
 9        GENE THEREOF
11 <130> FILE REFERENCE: 55022 (71526)
13 <140> CURRENT APPLICATION NUMBER: 09/646,825
14 <141> CURRENT FILING DATE: 2000-09-22
16 <150> PRIOR APPLICATION NUMBER: JP/10-96637
17 <151> PRIOR FILING DATE: 1998-03-24
19 <160> NUMBER OF SEQ ID NOS: 38
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2092
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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34 <222> LOCATION: (20)..(2077)
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41 atc tct ttc ttc gct aca gtc caa tcg agc gct aca ctc atc tcc act  100
42 Ile Ser Phe Phe Ala Thr Val Gln Ser Ser Ala Thr Leu Ile Ser Thr
43             15                  20                  25
45 tca tgc att tct cag gct gca ctg tac cag ttc gga tgc tca agc aag  148
46 Ser Cys Ile Ser Gln Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys
47         30                  35                  40
49 tca aag tct tgc tac tgc aag aac atc aat tgg ctc gga agc gtc act  196
50 Ser Lys Ser Cys Tyr Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr
51     45                  50                  55
53 gca tgc gct tat gag aac tcc aaa tct aac aag act ctg gac tcc gct  244
54 Ala Cys Ala Tyr Glu Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala
55 60                  65                  70                  75
57 ttg atg aaa ctt gcc agc caa tgc tca agt atc aag gtt tac aca ctg  292
58 Leu Met Lys Leu Ala Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr Leu
59                 80                  85                  90
61 gag gac atg aag aac atc tac ctt aat gca agt aac tac ctt cgc gct  340
62 Glu Asp Met Lys Asn Ile Tyr Leu Asn Ala Ser Asn Tyr Leu Arg Ala
63                 95                  100                 105
65 cct gag aaa tcc gat aag aag aca gtt gtt tca caa ccg ttg atg gca  388
66 Pro Glu Lys Ser Asp Lys Lys Thr Val Val Ser Gln Pro Leu Met Ala
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67          110                 115                 120
69 aat gag acg gcc tat cac tac tac tat gag gaa aac tat ggg atc cac    436
70 Asn Glu Thr Ala Tyr His Tyr Tyr Tyr Glu Glu Asn Tyr Gly Ile His
71     125                 130                 135
73 ttg aat ttg atg cga tct caa tgg tgc gca tgg ggc ctc gtc ttc ttc    484
74 Leu Asn Leu Met Arg Ser Gln Trp Cys Ala Trp Gly Leu Val Phe Phe
75 140                 145                 150                 155
77 tgg gtc gca gtc ctt acc gcc gca act atc ttg aac att ctc aaa cgc    532
78 Trp Val Ala Val Leu Thr Ala Ala Thr Ile Leu Asn Ile Leu Lys Arg
79                 160                 165                 170
81 gta ttc ggc aag aac att atg gca aat tct gtt aag aag tct ctt atc    580
82 Val Phe Gly Lys Asn Ile Met Ala Asn Ser Val Lys Lys Ser Leu Ile
83             175                 180                 185
85 tac cca agc gtt tac aaa gac tac aac gag aga act ttc tat ctt tgg    628
86 Tyr Pro Ser Val Tyr Lys Asp Tyr Asn Glu Arg Thr Phe Tyr Leu Trp
87         190                 195                 200
89 aaa cgt ttg cca ttc aac ttt aca act cga ggc aaa gga ctc gta gtt    676
90 Lys Arg Leu Pro Phe Asn Phe Thr Thr Arg Gly Lys Gly Leu Val Val
91     205                 210                 215
93 ctt atc ttt gtc att ctg act att ctc tca ctc tct ttc gga cat aac    724
94 Leu Ile Phe Val Ile Leu Thr Ile Leu Ser Leu Ser Phe Gly His Asn
95 220                 225                 230                 235
97 atc aag ttg cca cat cct tac gat aga cct aga tgg aga aga tca atg    772
98 Ile Lys Leu Pro His Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met
99                 240                 245                 250
101 gca ttc gtc tca cgc cgt gct gac ttg atg gca atc gct ctt ttc ccc   820
102 Ala Phe Val Ser Arg Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro
103             255                 260                 265
105 gtg gtg tac ctt ttc ggt atc cgg aac aac ccc ttc atc cca atc acc   868
106 Val Val Tyr Leu Phe Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr
107         270                 275                 280
109 gga ttg agc ttt agt act ttc aac ttt tac cac aaa tgg tca gca tac   916
110 Gly Leu Ser Phe Ser Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr
111     285                 290                 295
113 gtc tgc ttc atg tta gcc gtc gtc cat tca atc gtt atg acc gct tca   964
114 Val Cys Phe Met Leu Ala Val Val His Ser Ile Val Met Thr Ala Ser
115 300                 305                 310                 315
117 gga gtt aaa cga gga gta ttc cag tct ctt gta agg aaa ttc tac ttc   1012
118 Gly Val Lys Arg Gly Val Phe Gln Ser Leu Val Arg Lys Phe Tyr Phe
119             320                 325                 330
121 aga tgg gga ata gta gcc aca att ctt atg tcc atc atc att ttc cag   1060
122 Arg Trp Gly Ile Val Ala Thr Ile Leu Met Ser Ile Ile Ile Phe Gln
123             335                 340                 345
125 tcc gag aag gtc ttc agg aac cga ggt tat gaa atc ttc tta ctt att   1108
126 Ser Glu Lys Val Phe Arg Asn Arg Gly Tyr Glu Ile Phe Leu Leu Ile
127             350                 355                 360
129 cac aaa gcc atg aac atc atg ttt atc ata gct atg tat tac cat tgc   1156
130 His Lys Ala Met Asn Ile Met Phe Ile Ile Ala Met Tyr Tyr His Cys
131     365                 370                 375
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Input Set  : A:\55022715.app
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133 cac aca cta gga tgg atg ggc tgg atc tgg tcc atg gct ggc atc ctc   1204
134 His Thr Leu Gly Trp Met Gly Trp Ile Trp Ser Met Ala Gly Ile Leu
135 380             385             390             395
137 tgc ttc gac agg ttc tgc cga att gta cgt atc atc atg aac gga ggt   1252
138 Cys Phe Asp Arg Phe Cys Arg Ile Val Arg Ile Ile Met Asn Gly Gly
139             400             405             410
141 ctt aag acc gcc act ttg tcg acc aca gat gat tct aac gtt atc aag   1300
142 Leu Lys Thr Ala Thr Leu Ser Thr Thr Asp Asp Ser Asn Val Ile Lys
143             415             420             425
145 atc tct gtc aag aag cct aag ttc ttc aag tat caa gtg gga gca ttt   1348
146 Ile Ser Val Lys Lys Pro Lys Phe Phe Lys Tyr Gln Val Gly Ala Phe
147             430             435             440
149 gcc tat atg tac ttt ctt tca cca aaa tca gcc tgg ttc tac agt ttt   1396
150 Ala Tyr Met Tyr Phe Leu Ser Pro Lys Ser Ala Trp Phe Tyr Ser Phe
151     445             450             455
153 caa tct cat ccc ttc aca gtc cta tca gaa agg cac aga gat cct aac   1444
154 Gln Ser His Pro Phe Thr Val Leu Ser Glu Arg His Arg Asp Pro Asn
155 460             465             470             475
157 aac cca gat caa cta act atg tac gtc aaa gct aac aag ggc att acg   1492
158 Asn Pro Asp Gln Leu Thr Met Tyr Val Lys Ala Asn Lys Gly Ile Thr
159             480             485             490
161 aga gta ctt ctt agc aaa gtt cta agc gct cca aac cat acc gtt gat   1540
162 Arg Val Leu Leu Ser Lys Val Leu Ser Ala Pro Asn His Thr Val Asp
163             495             500             505
165 tgc aag att ttc tta gag gga cca tat ggc gta act gtc cct cac att   1588
166 Cys Lys Ile Phe Leu Glu Gly Pro Tyr Gly Val Thr Val Pro His Ile
167             510             515             520
169 gcc aaa ctt aag aga aat cta gta gga gta gct gcg ggc ctc ggc gtg   1636
170 Ala Lys Leu Lys Arg Asn Leu Val Gly Val Ala Ala Gly Leu Gly Val
171     525             530             535
173 gca gcc atc tac ccc cat ttc gta gaa tgc ctt aga ttg cct agc act   1684
174 Ala Ala Ile Tyr Pro His Phe Val Glu Cys Leu Arg Leu Pro Ser Thr
175 540             545             550             555
177 gat caa ctg cag cac aag ttc tac tgg atc gtc aac gac ctt agt cac   1732
178 Asp Gln Leu Gln His Lys Phe Tyr Trp Ile Val Asn Asp Leu Ser His
179             560             565             570
181 ctt aag tgg ttc gaa aac gag cta caa tgg ctt aag gag aaa tct tgt   1780
182 Leu Lys Trp Phe Glu Asn Glu Leu Gln Trp Leu Lys Glu Lys Ser Cys
183             575             580             585
185 gaa gtc tct gtc atc tac act ggg tca tca gtg gag gat aca aac tca   1828
186 Glu Val Ser Val Ile Tyr Thr Gly Ser Ser Val Glu Asp Thr Asn Ser
187             590             595             600
189 gat gag tcc act aag ggt ttc gat gac aag gaa gaa tct gaa atc acc   1876
190 Asp Glu Ser Thr Lys Gly Phe Asp Asp Lys Glu Glu Ser Glu Ile Thr
191 605             610             615
193 gta gaa tgc ctt aac aag agg cca gac ctc aaa gag cta gtg aga tca   1924
194 Val Glu Cys Leu Asn Lys Arg Pro Asp Leu Lys Glu Leu Val Arg Ser
195 620             625             630             635
197 gag atc aaa ttg tca gaa ctc gag aac aac aac atc act ttc tac tca   1972
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Input Set : A:\55022715.app
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198 Glu Ile Lys Leu Ser Glu Leu Glu Asn Asn Asn Ile Thr Phe Tyr Ser
199             640             645             650
201 tgc gga cca gcg act ttc aat gac gac ttt agg aat gca gtt gta caa     2020
202 Cys Gly Pro Ala Thr Phe Asn Asp Asp Phe Arg Asn Ala Val Val Gln
203             655             660             665
205 ggt atc gat tct agt ctg aag ata gat gtc gaa cta gag gag gag agt     2068
206 Gly Ile Asp Ser Ser Leu Lys Ile Asp Val Glu Leu Glu Glu Glu Ser
207             670             675             680
209 ttt act tgg taagagctca agctt                                        2092
210 Phe Thr Trp
211     685
214 <210> SEQ ID NO: 2
215 <211> LENGTH: 686
216 <212> TYPE: PRT
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220 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
221       saccharomyces cerevisiae
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224 Met Val Arg Thr Arg Val Leu Phe Cys Leu Phe Ile Ser Phe Phe Ala
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228             20              25              30
230 Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys Ser Lys Ser Cys Tyr
231         35              40              45
233 Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr Ala Cys Ala Tyr Glu
234     50              55              60
236 Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala Leu Met Lys Leu Ala
237  65              70              75              80
239 Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr Leu Glu Asp Met Lys Asn
240             85              90              95
242 Ile Tyr Leu Asn Ala Ser Asn Tyr Leu Arg Ala Pro Glu Lys Ser Asp
243             100             105             110
245 Lys Lys Thr Val Val Ser Gln Pro Leu Met Ala Asn Glu Thr Ala Tyr
246         115             120             125
248 His Tyr Tyr Tyr Glu Glu Asn Tyr Gly Ile His Leu Asn Leu Met Arg
249     130             135             140
251 Ser Gln Trp Cys Ala Trp Gly Leu Val Phe Phe Trp Val Ala Val Leu
252 145             150             155             160
254 Thr Ala Ala Thr Ile Leu Asn Ile Leu Lys Arg Val Phe Gly Lys Asn
255             165             170             175
257 Ile Met Ala Asn Ser Val Lys Lys Ser Leu Ile Tyr Pro Ser Val Tyr
258             180             185             190
260 Lys Asp Tyr Asn Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe
261         195             200             205
263 Asn Phe Thr Thr Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile
264     210             215             220
266 Leu Thr Ile Leu Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His
267 225             230             235             240
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PATENT APPLICATION:   US/09/646,825     TIME: 15:59:57

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269 Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met Ala Phe Val Ser Arg
270             245             250             255
272 Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro Val Val Tyr Leu Phe
273             260             265             270
275 Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr Gly Leu Ser Phe Ser
276         275             280             285
278 Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr Val Cys Phe Met Leu
279     290             295             300
281 Ala Val Val His Ser Ile Val Met Thr Ala Ser Gly Val Lys Arg Gly
282 305             310             315             320
284 Val Phe Gln Ser Leu Val Arg Lys Phe Tyr Phe Arg Trp Gly Ile Val
285             325             330             335
287 Ala Thr Ile Leu Met Ser Ile Ile Ile Phe Gln Ser Glu Lys Val Phe
288         340             345             350
290 Arg Asn Arg Gly Tyr Glu Ile Phe Leu Leu Ile His Lys Ala Met Asn
291         355             360             365
293 Ile Met Phe Ile Ile Ala Met Tyr Tyr His Cys His Thr Leu Gly Trp
294     370             375             380
296 Met Gly Trp Ile Trp Ser Met Ala Gly Ile Leu Cys Phe Asp Arg Phe
297 385             390             395             400
299 Cys Arg Ile Val Arg Ile Ile Met Asn Gly Gly Leu Lys Thr Ala Thr
300             405             410             415
302 Leu Ser Thr Thr Asp Asp Ser Asn Val Ile Lys Ile Ser Val Lys Lys
303         420             425             430
305 Pro Lys Phe Phe Lys Tyr Gln Val Gly Ala Phe Ala Tyr Met Tyr Phe
306         435             440             445
308 Leu Ser Pro Lys Ser Ala Trp Phe Tyr Ser Phe Gln Ser His Pro Phe
309     450             455             460
311 Thr Val Leu Ser Glu Arg His Arg Asp Pro Asn Asn Pro Asp Gln Leu
312 465             470             475             480
314 Thr Met Tyr Val Lys Ala Asn Lys Gly Ile Thr Arg Val Leu Leu Ser
315         485             490             495
317 Lys Val Leu Ser Ala Pro Asn His Thr Val Asp Cys Lys Ile Phe Leu
318         500             505             510
320 Glu Gly Pro Tyr Gly Val Thr Val Pro His Ile Ala Lys Leu Lys Arg
321     515             520             525
323 Asn Leu Val Gly Val Ala Ala Gly Leu Gly Val Ala Ala Ile Tyr Pro
324     530             535             540
326 His Phe Val Glu Cys Leu Arg Leu Pro Ser Thr Asp Gln Leu Gln His
327 545             550             555             560
329 Lys Phe Tyr Trp Ile Val Asn Asp Leu Ser His Leu Lys Trp Phe Glu
330         565             570             575
332 Asn Glu Leu Gln Trp Leu Lys Glu Lys Ser Cys Glu Val Ser Val Ile
333         580             585             590
335 Tyr Thr Gly Ser Ser Val Glu Asp Thr Asn Ser Asp Glu Ser Thr Lys
336     595             600             605
338 Gly Phe Asp Asp Lys Glu Glu Ser Glu Ile Thr Val Glu Cys Leu Asn
339     610             615             620
341 Lys Arg Pro Asp Leu Lys Glu Leu Val Arg Ser Glu Ile Lys Leu Ser
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**VERIFICATION SUMMARY**
PATENT APPLICATION:  US/09/646,825

DATE: 03/29/2001
TIME: 15:59:58

Input Set : **A:\55022715.app**
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